



SEQUENCE LISTING

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<110> Behan, Dominic P.  
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Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln  
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Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile  
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Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu  
245 250 255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
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Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
275 280 285

Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
405 410 415

Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser  
420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala  
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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
 35 40 45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
 50 55 60

Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
 65 70 75 80

Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
85 90 95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
100 105 110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
115 120 125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
130 135 140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
145 150 155 160

Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu  
165 170 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe  
180 185 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
195 200 205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
225 230 235 240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
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Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val  
260 265 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg  
275 280 285

Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val  
290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser  
305 310 315 320

Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala  
325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln  
340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu  
355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys  
370 375 380

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385 390 395 400

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<400> 14

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Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His  
35 40 45

Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val  
50 55 60

Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp  
65 70 75 80

Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu  
85 90 95

Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg  
100 105 110

Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly  
115 120 125

Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe  
130 135 140

Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu  
145 150 155 160

Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala  
Page 19

165

170

175

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr  
180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser  
195 200 205

Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys  
210 215 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala  
225 230 235 240

Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys  
245 250 255

Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile  
260 265 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His  
275 280 285

Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser  
290 295 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser  
305 310 315 320

Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys  
325 330 335

Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe  
340 345 350

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala  
355 360 365

Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His  
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Ser Arg Ser Val Ser Ser  
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35 40 45

Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp  
50 55 60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg  
65 70 75 80

Arg Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys  
85 90 95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu  
100 105 110

Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg  
115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val  
130 135 140

Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu  
145 150 155 160

Asp Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg  
165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val

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185

190

Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile  
195 200 205

His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser  
210 215 220

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala  
225 230 235 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val  
245 250 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val  
260 265 270

Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala  
275 280 285

Val Thr Leu Leu Phe Leu Leu Trp Gly Pro Tyr Val Val Ala Ser  
290 295 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu  
305 310 315 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val  
325 330 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln  
340 345 350

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355 360 365

Asp Leu Lys Gly Ile Gly Leu  
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<212> PRT

<213> Homo sapiens

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Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe			
35	40	45	

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr			
50	55	60	

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu			
65	70	75	80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg

85

90

95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu  
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu  
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile  
130 135 140

Phe Ile Trp Phe Phe Leu Phe Ile Ser Leu Pro Asn Thr Ile Leu  
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu  
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys  
180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val  
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys  
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val  
225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro  
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn  
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn  
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr  
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Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln  
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Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly

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25

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Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu  
35 40 45

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu  
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Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu  
65 70 75 80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys  
85 90 95

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe  
100 105 110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His  
115 120 125

Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile  
130 135 140

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe  
145 150 155 160

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe  
165 170 175

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met  
180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu  
195 200 205

Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro  
210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln  
225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro  
245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu

260

265

270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe  
275 280 285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val  
290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg  
305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn  
325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr  
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aaagtttcc tccctgtatt cctcacaata gcttcgtca ttggacttgc aggcaattcc 180  
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ctgaatttgg ctgttagcaga tttactcattt ctattcactc tgccttttg ggctgttaat 300  
gcagttcatg ggtgggtttt agggaaaata atgtcaaaa taacttcagc cttgtacaca 360  
ctaaactttg tctctggaat gcagttctg gcttgcata gcatagacag atatgtggca 420  
gtaactaatg tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480  
gtctggatgg ctgccatctt gctgagcata cccagctgg tttttatac agtaaatgac 540  
aatgcttagt gcattccat tttccccgc tacctaggaa catcaatgaa agcattgatt 600  
caaatgctag agatctgcat tggatttgta gtaccctttc ttattatggg ggtgtgctac 660  
tttatcacgg caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720

gttctgctca cagtcgttat agtttcatt gtcactcaac tgccttataa cattgtcaag 780  
ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840  
atggacatcg ccatccaagt cacagaaagc attgcactct ttcacagctg cctcaaccca 900  
atccttatg ttttatggg agcatcttc aaaaactacg ttatgaaagt ggccaagaaa 960  
tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttcctttga ttctgaggg 1020  
cctacagagc caaccagtagc ttttagcatt taa 1053

<210> 24  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 24

Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn  
1 5 10 15

Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile  
20 25 30

Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu  
35 40 45

Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala  
50 55 60

Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile  
65 70 75 80

Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe  
85 90 95

Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys  
100 105 110

Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln  
115 120 125

Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val  
130 135 140

Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys  
145 150 155 160

Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr  
165 170 175

Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu  
180 185 190

Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly  
195 200 205

Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala  
210 215 220

Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys  
225 230 235 240

Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr  
245 250 255

Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile  
260 265 270

Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr  
275 280 285

Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val  
290 295 300

Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys  
305 310 315 320

Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe  
325 330 335

Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile  
340 345 350

<210> 25  
<211> 1116  
<212> DNA  
<213> Homo sapiens

<400> 25  
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gccaagacct gcaacaacgt gtccttcgaa gagagcagga tagtcctgggt cgtggtgtac 120  
agcgcggtgt gcaacgctggg ggtgccggcc aactgcctga ctgcgtggct ggcgctgctg 180

caggtactgc	agggcaacgt	gctggccgtc	tacctgctct	gcctggcact	ctgcgaactg	240
ctgtacacag	gcacgctgcc	actctgggtc	atctatatcc	gcaaccagca	ccgctggacc	300
ctaggcctgc	tggcctcgaa	ggtgaccgccc	tacatcttct	tctgcaacat	ctacgtcagc	360
atcctcttcc	tgtgctgcat	ctcctgcgac	cgcttcgtgg	ccgtgggtga	cgcgctggag	420
agtcggggcc	gccgcccggc	gaggaccgccc	atcctcatct	ccgcctgcat	cttcatcctc	480
gtcgggatcg	ttcactaccc	ggtgttccag	acggaagaca	aggagacctg	ctttgacatg	540
ctgcagatgg	acagcaggat	tgccgggtac	tactacgcca	ggttcaccgt	tggcttgcc	600
atccctctct	ccatcatcgc	ttcaccaac	caccggattt	tcaggagcat	caagcagagc	660
atgggcttaa	gcgctgccc	gaaggccaag	gtgaagcact	cggccatcgc	ggtgggtgtc	720
atcttcctag	tctgcttcgc	cccgtaccac	ctgggtctcc	tcgtcaaagc	cgctgcctt	780
tcctactaca	gaggagacag	gaacgcccatt	tgcggcttgg	aggaaaggct	gtacacagcc	840
tctgtggtgt	ttctgtgcct	gtccacggtg	aacggcgtgg	ctgacccat	tatctacgtg	900
ctggccacgg	accattcccg	ccaagaagtg	tccagaatcc	ataaggggtg	gaaagagtg	960
tccatgaaga	cagacgtcac	caggctcacc	cacagcaggg	acaccgagga	gctgcagtcg	1020
cccgtggccc	ttgcagacca	ctacaccc	tccaggcccg	tgcacccacc	agggtcacca	1080
tgccctgcaa	agaggctgat	tgaggagtcc	tgctga			1116

<210> 26  
 <211> 371  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 26

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser  
 1 5 10 15

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser  
 20 25 30

Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val  
 35 40 45

Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln  
 50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu  
 65 70 75 80

Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln  
85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile  
100 105 110

Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser  
115 120 125

Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg  
130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu  
145 150 155 160

Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr  
165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr  
180 185 190

Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe  
195 200 205

Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser  
210 215 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
225 230 235 240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
260 265 270

Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
290 295 300

His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
305 310 315 320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
340 345 350

Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu  
355 360 365

Glu Ser Cys  
370

<210> 27  
<211> 1113  
<212> DNA  
<213> Homo sapiens

<400> 27  
atggcgaact atagccatgc agctgacaac attttgcaaa atctctcgcc tctaacagcc 60  
tttctgaaac tgacttcctt gggtttcata ataggagtca gcgtgggtggg caaccccttg 120  
atctccattt tgcttagtgaa agataagacc ttgcatacgag caccttacta cttcctgttg 180  
gatctttgct gttcagatat cctcagatct gcaatttgtt tcccatttgt gttcaactct 240  
gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaagtgtat tgcctttctg 300  
ggggtttgtt cctgtttcca cactgcttcc atgctcttct gcatcagtgt caccagatac 360  
ttagctatcg cccatcacccg cttctataca aagaggctga cctttggac gtgtctggct 420  
gtgatctgta tggtgtggac tctgtctgtg gccatggcat ttccccgggt ttttagacgtg 480  
ggcacttact cattcattag ggaggaagat caatgcaccc tccaaacacccg ctccttcagg 540  
gctaattgatt ccttaggatt tatgctgctt ctgtctctca tcctccttagc cacacagctt 600  
gtctacctca agctgatatt tttcgccac gatcgaagaa aaatgaagcc agtccagtt 660  
gtagcagcag tcagccagaa ctggactttt catggctctg gagccagtgg ccaggcagct 720  
gccaattggc tagcaggatt tggaaagggtt cccacaccac ccacccgtt gggcatcagg 780  
caaaatgcaa acaccacagg cagaagaagg ctattggct tagacgagtt caaaatggag 840  
aaaagaatca gcagaatgtt ctatataatg acttttctgt ttctaacctt gtggggcccc 900  
tacctgggtgg cctgttattt gagagttttt gcaagaggc ctgttagtacc agggggattt 960  
ctaacagctg ctgtctggat gagtttgcc caagcaggaa tcaatcctt tgcatt 1020  
ttctcaaaaca gggagctgag gcgctgtttc agcacaaccc ttctttactg cagaaaatcc 1080  
aggttaccaa gggAACCTTA ctgtgttata tga 1113

<210> 28  
<211> 370  
<212> PRT  
<213> Homo sapiens

<400> 28

Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser  
1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly  
20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp  
35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys  
50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser  
65 70 75 80

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val  
85 90 95

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu  
100 105 110

Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe  
115 120 125

Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met  
130 135 140

Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val  
145 150 155 160

Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His  
165 170 175

Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Ala  
180 185 190

Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe  
195 200 205

Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val  
210 215 220

Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala  
225 230 235 240

Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu  
245 250 255

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu  
260 265 270

Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr  
275 280 285

Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala  
290 295 300

Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe  
305 310 315 320

Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro  
325 330 335

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr  
340 345 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys  
355 360 365

Val Ile  
370

<210> 29  
<211> 1080  
<212> DNA  
<213> Homo sapiens

<400> 29  
atgcagggtcc cgaacagcac cggccggac aacgcgacgc tgcagatgct gcgaaacccg 60  
gcgatcgccgg tggccctgcc cgtgggtac tcgctgggtgg cggcggtcag catccgggc 120  
aacaccttct ctctgtgggt gctgtgccgg cgcattggggc ccagatcccc gtcgggtcatc 180  
ttcatgatca acctgagcgt cacggacctg atgctggcca gcgtgttgcc tttccaaatc 240  
tactaccatt gcaaccgcca ccactgggta ttcggggtgc tgcttgcaa cgtgggtgacc 300

gtggccttt acgcaaacat gtattccagc atcctcacca tgacctgtat cagcgtggag	360
cgcttcctgg gggtcctgta cccgctcagc tccaagcgct ggcgccgccc tcgttacgcg	420
gtggccgcgt gtgcagggac ctggctgctg ctcctgaccg ccctgtgccc gctggcgcgc	480
accgatctca cctacccggt gcacgcctg ggcacatcatca cctgcttcga cgtcctcaag	540
tggacgatgc tccccagcgt ggccatgtgg gccgtgtcc tcttcaccat cttcatcctg	600
ctgttcctca tcccgttcgt gatcaccgtg gcttgttaca cggccaccat cctcaagctg	660
ttgcgcacgg aggaggcgca cggccggag cagcggaggc gcgcgggtggg cctggccgcg	720
gtggtcttgc tggccttgcgt cacctgcttc gcccccaaca acttcgtgct cctggcgcac	780
atcgtgagcc gcctgttcta cggcaagagc tactaccacg tgtacaagct cacgctgtgt	840
ctcagctgcc tcaacaactg tctggaccgg tttgtttatt actttgcgtc ccggaaattc	900
cagctgcgccc tgcggaaata tttgggctgc cgccgggtgc ccagagacac cctggacacg	960
cggccgcgaga gcctttctc cgccaggacc acgtccgtgc gctccgagggc cggcgcac	1020
cctgaaggga tggagggagc caccaggccc ggcctccaga ggcaggagag tgtgttctga	1080

<210> 30

<211> 359

<212> PRT

<213> Homo sapiens

<400> 30

Met	Gln	Val	Pro	Asn	Ser	Thr	Gly	Pro	Asp	Asn	Ala	Thr	Leu	Gln	Met
1								5			10				15

Leu	Arg	Asn	Pro	Ala	Ile	Ala	Val	Ala	Leu	Pro	Val	Val	Tyr	Ser	Leu
					20			25					30		

Val	Ala	Ala	Val	Ser	Ile	Pro	Gly	Asn	Leu	Phe	Ser	Leu	Trp	Val	Leu
					35			40				45			

Cys	Arg	Arg	Met	Gly	Pro	Arg	Ser	Pro	Ser	Val	Ile	Phe	Met	Ile	Asn
			50			55				60					

Leu	Ser	Val	Thr	Asp	Leu	Met	Leu	Ala	Ser	Val	Leu	Pro	Phe	Gln	Ile
					65		70			75				80	

Tyr	Tyr	His	Cys	Asn	Arg	His	His	Trp	Val	Phe	Gly	Val	Leu	Leu	Cys
					85			90				95			

Asn	Val	Val	Thr	Val	Ala	Phe	Tyr	Ala	Asn	Met	Tyr	Ser	Ser	Ile	Leu

100

105

110

Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro  
115 120 125

Leu Ser Ser Lys Arg Trp Arg Arg Arg Tyr Ala Val Ala Ala Cys  
130 135 140

Ala Gly Thr Trp Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg  
145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu

340

345

350

Gln Arg Gln Glu Ser Val Phe  
 355

<210> 31  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
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 ccagtcggcg ccggggcgcg ctccggtgcc gcggcgagtgc acaggctg gcagccatgg 120  
 gctgagtgcc cgggacccaa ggggaggggg caactgctgg cgaccgccc cccttgcgt 180  
 cgctggcccg cccctcgcc tgccagctcc agcccccgc ccggagcgcc gtccgctcac 240  
 tcggttcaag gcagcgac tgcgggtggc gcacgaccag ggccgagacc ttggggcg 300  
 cggccatgg agtcgggct gctgcggcg gcgcgggtga gcgaggtcat cgtcctgcac 360  
 tacaactaca ccggcaagct ccgcggtgac agctaccagc cgggtgccc cctgcgcgc 420  
 gacgcgtgg tgtgcctggc ggtgtgcgc ttcatgtgc tagagaatct agccgtgtt 480  
 ttgggtctcg gacgccaccc gcgcctccac gctccatgt tcctgctcct gggcagcctc 540  
 acgttgtcgg atctgctggc aggccgcgc tacgcccaca acatcctact gtcggggccg 600  
 ctcacgctga aactgtcccc cgcgctctgg ttcgcacggg agggaggcgt ctgcgtggca 660  
 ctcactgcgt ccgtgctgag ctcctggcc atcgcgtgg agcgcagcct caccatggcg 720  
 cgcagggggc ccgcgcgcgt ctccagtcgg gggcgacgc tggcgatggc agccgcggcc 780  
 tggggcgtgt cgctgctcct cgggcctcgt ccagcgctgg gctggaaattg cttgggtcgc 840  
 ctggacgctt gtcactgt cttgcgcctc tacgccaagg cctacgtgtc cttctgcgtg 900  
 ctcgccttcg tgggcattcct ggccgcgatc tgtgcactct acgcgcgcac ctactgccag 960  
 gtacgcgcaca acgcgcggcg ctcgcggca cggccggga ctgcggggac cacctcgacc 1020  
 cgggcgcgac gcaagccgcg ctctctggcc ttgctgcgcac cgcgcgt ggtgctcctg 1080  
 gcctttgtgg catgttgggg ccccttcctc ctgctgctgt tgctcgacgt ggcgtgccc 1140  
 ggcgcacact gtcctgtact ctcgcaggcc gatcccttcc tggactggc catggccaac 1200  
 tcacttctga accccatcat ctacacgcac accaaccgcg acctgcgcac cgcgcctc 1260  
 cgcctggctc gtcggacg ccactcctgc ggcagagacc cgcgtggc ccagcgtcg 1320  
 gcgagcgcgg ctgaggctc cggggcctg cgcgcgtgcc tgccccggg cttgtatggg 1380  
 agcttcagcg gtcggagcg ctcatgcac cagcgcacgc ggctggacac cagcggctcc 1440

acaggcagcc ccgggtgcacc cacagccgcc cgactctgg tatcagaacc ggctgcagac 1500  
 tga 1503

<210> 32  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 32

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu  
 1 5 10 15

Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala  
 20 25 30

Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly  
 35 40 45

Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala  
 50 55 60

Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His  
 65 70 75 80

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg  
 85 90 95

Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro  
 100 105 110

Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg  
 115 120 125

Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val  
 130 135 140

Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu  
 145 150 155 160

Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu  
 165 170 175

Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala  
 180 185 190

Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala  
195 200 205

Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser  
210 215 220

Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala  
225 230 235 240

Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met  
245 250 255

Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala  
260 265 270

Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu  
275 280 285

Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val  
290 295 300

Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln  
305 310 315 320

Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly  
325 330 335

Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu  
340 345 350

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro  
355 360 365

Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys  
370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn  
385 390 395 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg  
405 410 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg  
420 425 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly  
435 440 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly  
450 455 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser  
465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu  
485 490 495

Pro Ala Ala Asp  
500

<210> 33  
<211> 1029  
<212> DNA  
<213> Homo sapiens

<400> 33  
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tacaaaatca cccaggtcct cttcccaactg ctctacactg tcctgtttt tgttggactt 120  
atcacaatg gcctggcgat gaggatttc tttcaaattcc ggagtaaatc aaactttatt 180  
attttctta agaacacagt catttctgat cttctcatga ttctgacttt tccattcaaa 240  
attcttagtg atgccaaact gggAACAGGA ccactgagaa cttttgtgtg tcaagttacc 300  
tccgtcatat tttatccac aatgtatatac agtatttcat tcctggact gataactatc 360  
gatcgctacc agaagaccac caggccattt aaaacatcca accccaaaaa tctttgggg 420  
gctaaagattc tctctgttgcatctggca ttcatgttct tactctctt gcctaacatg 480  
attctgacca acaggcagcc gagagacaag aatgtgaaga aatgctctt cttaaatca 540  
gagttcggc tagtctggca taaaatagta aattacatct gtcaagtcat ttctggatt 600  
aatttcttaa ttgttattgt atgttataca ctcattacaa aagaactgta ccggcatac 660  
gtaagaacga ggggtgttagg taaagtcccc agaaaaagg tgaacgtcaa agttttcatt 720  
atcattgctg tattctttat ttgtttgtt ccttccatt ttgcccgaat tccttacacc 780  
ctgagccaa cccggatgt ctgtactgc actgctgaaa atactctgtt ctatgtgaaa 840  
gagagcactc tgggttaac ttccattaaat gcatgcctgg atccgttcat ctatttttc 900  
ctttgcaagt cttcagaaa ttccattgata agtatgctga agtgcggcaa ttctgcaaca 960  
tctctgtccc aggacaatag gaaaaagaa caggatggtg gtgaccggaa tgaagagact 1020

ccaatgtaa

1029

<210> 34  
<211> 342  
<212> PRT  
<213> Homo sapiens  
  
<400> 34

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu  
1 5 10 15

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr  
20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg  
35 40 45

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys  
50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys  
65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val  
85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile  
100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg  
115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu  
130 135 140

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met  
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser  
165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr  
180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys

195 200

205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg  
210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile  
225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg  
245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala  
260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser  
275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser  
290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr  
305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro  
325 330 335

Asn Glu Glu Thr Pro Met  
340

<210> 35  
<211> 1077  
<212> DNA  
<213> Homo sapiens

<400> 35  
atgtcggtct gctaccgtcc cccagggAAC gagacactgc tgagctggaa gacttcgcgg 60  
gccacaggca cagccttcct gctgctggcg gcgctgctgg ggctgcctgg caacggcttc  
gtgggtgtgga gcttggcgGGG ctggcgccct gcacgggggc gaccgctggc ggccacgctt 120  
gtgctgcacc tggcgctggc cgacggcgcg gtgctgctgc tcacccgct ctttgtggcc  
ttcctgaccc ggcaggcctg gccgctggc caggcgccgt gcaaggcggt gtactacgtg 180  
tgcgcgctca gcatgtacgc cagcgtgctg ctcaccggcc tgctcagcct gcagcgctgc  
ctcgcagtca cccgcccctt cctggcgccct cggtcgccca gcccggccct ggcccgccgc 240  
ctgctgctgg cggtctggct ggccgcctg ttgctcgccg tcccgccgc cgtctaccgc 300  
360 420 480

cacctgtgga	gggaccgcgt	atgccagctg	tgccacccgt	cgccggtcca	cgccgcccgc	540
cacctgagcc	tggagactct	gaccgcttgc	gtgcttcctt	tcgggctgat	gctcggtgc	600
tacagcgtga	cgctggcacg	gctgcggggc	gcccgcgtgg	gctccgggcg	gcacggggcg	660
cgggtgggcc	ggctgggtgag	cgccatcgtg	cttgccttcg	gcttgctctg	ggcccccctac	720
cacgcagtca	accttctgca	ggcggtcgca	gcgctggctc	caccggaagg	ggccttggcg	780
aagctggcg	gagccggcca	ggcggcgca	gccccgaacta	cgcccttggc	cttcttcagt	840
tctagcgtca	acccgggtgct	ctacgtcttc	accgctggag	atctgctgcc	ccggggcaggt	900
ccccgttcc	tcacgcggct	cttcaaggc	tctggggagg	cccgaggggg	cgcccgctct	960
aggaaaggga	ccatggagct	ccgaactacc	cctcagctga	aagtggtggt	gcagggccgc	1020
ggcaatggag	acccgggggg	tggatggag	aaggacggtc	cggaatggga	cctttga	1077

<210> 36  
 <211> 358  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 36

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp  
 1 5 10 15

Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu  
 20 25 30

Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp  
 35 40 45

Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu  
 50 55 60

Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala  
 65 70 75 80

Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala  
 85 90 95

Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr  
 100 105 110

Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu  
 115 120 125

Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala  
130 135 140

Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg  
145 150 155 160

His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val  
165 170 175

His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu  
180 185 190

Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu  
195 200 205

Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg  
210 215 220

Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr  
225 230 235 240

His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu  
245 250 255

Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly  
260 265 270

Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr  
275 280 285

Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu  
290 295 300

Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser  
305 310 315 320

Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val  
325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp  
340 345 350

Gly Pro Glu Trp Asp Leu  
355

<210> 37  
<211> 1005  
<212> DNA  
<213> Homo sapiens

<400> 37  
atgctgggaa tcatggcatg gaatgcaact tgcaaaaact ggctggcagc agaggctgcc 60  
ctggaaaagt actaccttc catttttat gggattgagt tcgttgcgg agtccttgg 120  
aataccattg ttgttacgg ctacatcttc tctctgaaga actggaacag cagtaatatt 180  
tatctctta acctctctgt ctctgactta gctttctgt gcaccctccc catgctgata 240  
aggagttatg ccaatggaaa ctggatataat ggagacgtgc tctgcataag caaccgata 300  
gtgcttcatg ccaacctcta taccaggatt ctcttctca cttttatcag catagatcga 360  
tacttgataa ttaagtatcc tttccgagaa caccttctgc aaaagaaaaga gtttgctatt 420  
ttaatctcct tggccatttg ggttttagta accttagagt tactacccat acttcccctt 480  
ataaatcctg ttataactga caatggcacc acctgtaatg atttgcaag ttctggagac 540  
cccaactaca acctcattta cagcatgtgt ctaacactgt tggggttcct tattcctctt 600  
tttgcgtatgt gtttctttta ttacaagatt gctctttcc taaagcagag gaataggcag 660  
gttgcgtactg ctctgcccct tgaaaagcct ctcaacttgg tcatcatggc agtggtaatc 720  
ttctctgtgc ttttacacc ctatcacgtc atgcggaatg tgaggatcgc ttcacgcctg 780  
gggagttgga agcagtatca gtgcactcag gtcgtcatca actcccttta cattgtgaca 840  
cggccttgg ctttctgaa cagtgtcatc aaccctgtct tctattttct tttggagat 900  
cacttcaggg acatgctgat gaatcaactg agacacaact tcaaatccct tacatccttt 960  
agcagatggg ctcatgaact cctacttca ttcagagaaa agtga 1005

<210> 38  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 38

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala  
1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile  
20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr  
35 40 45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn  
 50 55 60  
 /  
 Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile  
 65 70 75 80  
 Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile  
 85 90 95  
 Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe  
 100 105 110  
 Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe  
 115 120 125  
 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu  
 130 135 140  
 Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu  
 145 150 155 160  
 Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala  
 165 170 175  
 Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr  
 180 185 190  
 Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr  
 195 200 205  
 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala  
 210 215 220  
 Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile  
 225 230 235 240  
 Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile  
 245 250 255  
 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val  
 260 265 270  
 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser  
 275 280 285

Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp  
290 295 300

Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe  
 305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys  
325 330

<210> 39  
<211> 1296  
<212> DNA  
<213> *Homo sapiens*

ctggctgaga atttccttt agacagtggg cattaa

1296

<210> 40  
<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 40

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg  
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg  
20 25 30

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu  
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala  
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr  
65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe  
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu  
100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro

195

200

205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val  
260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Leu Lys Arg His Leu Ala Leu  
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
420 425 430

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 41  
ctgtgtacag cagttcgca agtg 24

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 42  
gagtgccagg cagagcagg agac 24

<210> 43  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 43  
cccgaaattcc tgcttgctcc cagcttggcc c 31

<210> 44  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 44  
tgtggatcct gctgtcaaag gtccattcc gg 32

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 45  
tcacaatgct aggtgtggc 20

<210> 46

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 46  
tgcatagaca atgggattac ag

22

<210> 47  
<211> 511  
<212> DNA  
<213> Homo sapiens

<400> 47  
tcacaatgct aggtgtggtc tggctggtgg cagtcatcg aggtcaccc atgtggcacg 60  
tgcaacaact tgagatcaa tatgacttcc tatatgaaaa ggaacacatc tgctgcttag 120  
aagagtggac cagccctgtg caccagaaga tctacaccac cttcatcctt gtcatcctct 180  
tcctcctgcc tcttatggtg atgcttattc tgtacgtaaa attggttatg aactttggat 240  
aaagaaaaga gttggggatg gttcagtgtc tcgaactatt catgaaaag aaatgtccaa 300  
aatagccagg aagaagaaac gagctgtcat tatgatggtg acagtggtgg ctctcttgc 360  
tgtgtgctgg gcaccattcc atgttgtcca tatgatgatt gaatacagta attttgaaaa 420  
ggaatatgat gatgtcacaa tcaagatgat ttttgctatc gtgcaaatttta ttggatttc 480  
caactccatc tgtaatccca ttgtctatgc a 511

<210> 48  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 48  
ctgcttagaa gagtggacca g

21

<210> 49  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 49  
ctgtgcacca gaagatctac ac

22

<210> 50	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 50	
caaggatgaa ggtgggttag a	21
<210> 51	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 51	
gtgttagatct tctggtgac acg	23
<210> 52	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 52	
gcaatgcagg tcatagtgag c	21
<210> 53	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 53	
tggagcatgg tgacggaaat gcagaag	27
<210> 54	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 54	
gtgtatgagca ggtcaactgag cgccaag	27

<210> 55  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 55  
gcaatgcagg cgcttaacat tac 23

<210> 56  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 56  
ttgggttaca atctgaaggg ca 22

<210> 57  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 57  
actccgtgtc cagcaggact ctg 23

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 58  
tgcgtgttcc tggaccctca cgtg 24

<210> 59  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 59  
caggccttgg atttaatgt cagggatgg 29

<210> 60  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Novel Sequence  
  
<400> 60  
ggagagtca g ctctgaaaga attcagg 27  
  
<210> 61  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Novel Sequence  
  
<400> 61  
tgatgtgatg ccagatacta atagcac 27  
  
<210> 62  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Novel Sequence  
  
<400> 62  
cctgattcat ttaggtgaga ttgagac 27  
  
<210> 63  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Novel Sequence  
  
<400> 63  
cccaagcttc cccaggtgta tttgat 26  
  
<210> 64  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Novel Sequence  
  
<400> 64  
gttggatcca cataatgcat tttctc 26

<210> 65  
<211> 1080  
<212> DNA  
<213> Homo sapiens

<400> 65  
atgatttctca actcttctac tgaagatgg attaaaagaa tccaaagatga ttgtccaaa 60  
gctggaaggc ataattacat atttgtcatg attcctactt tatacagttt catctttgt 120  
gtggaaatat ttggaaacag cttgggtgt atagtcattt acttttatat gaagctgaag 180  
actgtggcca gtgttttct tttgaattta gcactggctg acttatgctt tttactgact 240  
ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300  
tgtaagattt cttcagccag cgtcagttt aacctgtacg ctgtgtgtt tctactcagc 360  
tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg cttcgacgc 420  
acaatgctt tagccaaagt cacctgcattt atcatttgc tgctggcagg cttggccagt 480  
ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagttgt 540  
gtttccattt atgagtccca aaattcaacc cttccgatag ggctggcct gaccaaaaat 600  
atactgggtt tcctgtttcc tttctgatc attcttacaa gttatactct tatttggaaag 660  
gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgtga tatttttaag 720  
ataattatgg caattgtgct tttcttttc tttcctgga ttccccacca aatattcact 780  
tttctggatg tattgattca actaggcattt atacgtgact gttagattgc agatatttg 840  
gacacggcca tgcctatcac catttgtata gcttattttt acaattgcct gaatccttt 900  
ttttatggct ttctgggaa aaaattaaa agatatttc tccagcttct aaaatatatt 960  
cccccaaaag ccaaatccca ctcaaaccctt tcaacaaaaa tgagcacgct ttcctaccgc 1020  
ccctcagata atgtaagctc atccaccaag aagcctgcac catgtttga gtttgagtga 1080

<210> 66  
<211> 359  
<212> PRT  
<213> Homo sapiens

<400> 66

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 67

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 67

accatggca gcccctggaa cggcagc

27

<210> 68

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 68

agaaccacca ccagcaggac gcggacggtc tgccggtag

39

<210> 69

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 69

gtccgcgtcc tgctggtagt ggttctggca tttataatt

39

<210> 70

<211> 33

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Novel Sequence		
<400> 70		
cctggatcct tatccatcg tcttcacgtt agc		33
<210> 71		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Novel Sequence		
<400> 71		
ctggaattct cctgccagca tggta		26
<210> 72		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Novel Sequence		
<400> 72		
gcaggatcct atattgcgtg ctctgtcccc		30
<210> 73		
<211> 999		
<212> DNA		
<213> Homo sapiens		
<400> 73		
atggtaact ccacccaccc tgggatgcac acttctctgc acctctggaa ccgcagcagt		60
tacagactgc acagcaatgc cagttagtcc cttggaaaag gctactctga tggagggtgc		120
tacgagcaac tttttgtctc tcctgaggtg tttgtgactc tgggtgtcat cagttgttgc		180
gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac		240
ttttcatct gcagcttggc tgtggctgat atgctggta gcgtttcaaa tggatcagaa		300
accattatca tcaccctatt aaacagtaca gatacggatg cacagatgg cacagttaat		360
attgataatg tcattgactc ggtgatctgt agtccttgc ttgcattccat ttgcagcctg		420
ctttcaatttgc cagtggacag gtactttact atcttctatg ctctccagta ccataacatt		480
atgacagtttgc agcgggttgg gatcagcata agttgtatct gggcagcttgc cacggttca		540
ggcattttgt tcatcatttgc ctcagatgtt agtgctgtca tcatctgcct catcaccatgt		600

ttcttcacca	tgctggctct	catggcttct	ctctatgtcc	acatgttcct	gatggccagg	660
cttcacatta	agaggattgc	tgtccctccc	ggcactggtg	ccatccgcca	aggtgccaat	720
atgaagggag	cgattacctt	gaccatcctg	attggcgct	ttgttgtctg	ctgggccccca	780
ttcttcctcc	acttaatatt	ctacatctct	tgtcctcaga	atccatattg	tgtgtgcctc	840
atgtctca	ttaacttgta	tctcatactg	atcatgtgta	attcaatcat	cgatcctctg	900
atttatgcac	tccggagtca	agaactgagg	aaaacttca	aagagatcat	ctgttgctat	960
ccccctggag	gcctttgtga	cttgtctagc	agatattaa			999

<210> 74  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 74

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp  
 1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly  
 20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro  
 35 40 45

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu  
 50 55 60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr  
 65 70 75 80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser  
 85 90 95

Asn Gly Ser Glu Thr Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr  
 100 105 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val  
 115 120 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala  
 130 135 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile  
 145 150 155 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala  
165 170 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala  
180 185 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met  
195 200 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys  
210 215 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn  
225 230 235 240

Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val  
245 250 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro  
260 265 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr  
305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
325 330

<210> 75  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 75  
ccgaagcttc gagctgagta aggcggcggg ct

32

<210> 76  
<211> 31

<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 76

gtggattca tttccctgc ctcaacccca a

31

<210> 77

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 77

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ctgtgccgcc cgggggcgcc ttcctcaac agcagcagtg tggcaacct cagctgcgag	120
ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcacttt	180
tacgcagtga tcttcctgat gagcgttgaa ggaaatatgc tcatacatgt ggtcctggaa	240
ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcaactggc agtcagcgac	300
ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc	360
atcttggca ccgtcatctg caaggcggtt tcctaccta tgggggtgtc tgtgagtgt	420
tccacgctaa gcctcggtgc catcgactg gagcgatata gcgcacatctg ccgaccactg	480
caggcacgag tgtggcagac gcgcctccac gcggctcgcg tgattgttagc cacgtggctg	540
ctgtccggac tactcatggt gccttacccc gtgtacactg tcgtcaacc agtggggcct	600
cgtgtgtgc agtgcgtgca tcgctggccc agtgcgcggg tccgcagac ctggccgtat	660
ctgctgcttc tgctttgtt ctcatccca ggtgtggta tggccgtggc ctacgggctt	720
atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgcacag cgacagccaa	780
agcagggtcc gaaaccaagg cgggctgcca gggctgttc accagaacgg gcgttgcgg	840
cctgagactg gcgcgggtgg caaagacagc gatggctgt acgtgcact tccacgttcc	900
cggcctgccc tggagctgac ggcgcgtacg gtcctgggc cgggatccgg ctccggccc	960
acccaggcca agctgctggc taagaagcgc gtgggtgcggaa tgggtgtgtt gatcggttgc	1020
cttttttttc tgtgttggtt gccagtttat agtgcacaaca cgtggcgccg ctttgcgttgc	1080
ccgggtgcac accgagact ctcgggtgt cctatctcc tcattactt gctgagctac	1140
gcctcggcct gtgtcaaccc cctgggtctac tgcttcatgc accgtcgctt tcgcccaggcc	1200
tgcctggaaa ctgcgtcg ctgcgtcccc cggcctccac gagctcgccc cagggtctt	1260
cccgatgagg accctccac tccctccatt gcttcgtgt ccaggcttag ctacaccacc	1320

atcagcacac tggccctgg ctga

1344

<210> 78

<211> 447

<212> PRT

<213> Homo sapiens

<400> 78

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly  
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser  
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
85 90 95

Ala Val Ser Asp Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu  
325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Ile Ser Thr Leu Gly Pro Gly  
435 440 445

<210> 79	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 79	
tgcaagctta aaaaggaaaa aatgaacagc	30
<210> 80	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 80	
taaggatccc ttcccttcaa aacatccttg	30
<210> 81	
<211> 1014	
<212> DNA	
<213> Homo sapiens	
<400> 81	
atgaacagca catgtattga agaacagcat gacctggatc actatttggtt tcccatgttt	60
tacatctttg tgattatagt cagcattcca gccaatattt gatctctgtg tgtgtctttc	120
ctgcaaccca agaaggaaag tgaacttagga atttacctct tcagtttgc actatcagat	180
ttactctatg cattaactct cccttatgg attgattata ctttggataa agacaactgg	240
actttctctc ctgccttggt caaaggagt gctttctca tgtacatgaa gttttacagc	300
agcacagcat tcctcacctg cattggcgtt gatcggtatt tggctgtgt ctacccttg	360
aagttttttt tcctaaggac aagaagaatt gcactcatgg tcagcctgtc catctggata	420
ttggaaacca tcttcaatgc tgtcatgtt gggaaagatg aaacagttgt tgaatattgc	480
gatgccgaaa agtctaattt tactttatgc tatgacaaat accctttaga gaaatggcaa	540
atcaacctca acttggtcag gacgtgtaca ggctatgcaa taccttgggt caccatcctg	600
atctgttaacc gaaaagtcta ccaagctgtg cgccacaata aagccacgga aaacaaggaa	660
aagaagagaa tcataaaaact acttgtcagc atcacagttt ctttgtctt atgctttact	720
ccctttcatg tcatgttgc gattcgctgc atttttagagc atgctgtgaa ctgcgaagac	780
cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacgggtgc attaacaagt	840

ttaaattgtg ttgctgatcc aattctgtac tgtttttta ccgaaacagg aagatatgtat 900  
atgttgaata tattaaaatt ctgcactggg aggtgtaata catcacaaag acaaagaaaa 960  
cgcatactt ctgtgtctac aaaagatact atgaaattag aggtccttga gtag 1014

<210> 82  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 82

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu  
1 5 10 15

Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn  
20 25 30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu  
35 40 45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala  
50 55 60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp  
65 70 75 80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met  
85 90 95

Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg  
100 105 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg  
115 120 125

Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile  
130 135 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys  
145 150 155 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu  
165 170 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr  
180 185 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln  
195 200 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile  
210 215 220

Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr  
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val  
245 250 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr  
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile  
275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile  
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys  
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu  
325 330 335

Glu

<210> 83  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 83  
caggaagaag aaacgagctg tcattatgtt ggtgacagtg 40

<210> 84  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 84  
cactgtcacc atcataatga cagctcggtt cttcttcctg 40

<210> 85  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 85  
ggccaccggc agaccaaacg cgtcctgctg 30

<210> 86  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 86  
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 87  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 87  
ggaaaagaag agaatcaaaa aactacttgt cagcatc 37

<210> 88  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 88  
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 89  
<211> 1080  
<212> DNA  
<213> Homo sapiens

<400> 89

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gtggaaatat	ttggaaacag	cttgggtgg	atagtcattt	acttttatat	gaagctgaag	180
actgtggcca	gtgttttct	tttgaattta	gcactggctg	actttagctt	tttactgact	240
ttgccactat	gggctgtcta	cacagctatg	gaataccgct	ggccctttgg	caattaccta	300
tgttaagattt	cttcagccag	cgtcagttc	aacctgtacg	ctagtgtgtt	tctactcag	360
tgtctcagca	ttgatcgata	cctggctatt	gttcacccaa	tgaagtcccg	ccttcgacgc	420
acaatgctt	tagccaaagt	cacctgcac	atcatttggc	tgctggcagg	cttggccagt	480
ttgccagcta	taatccatcg	aaatgtattt	ttcattgaga	acaccaatat	tacagttgt	540
gctttccatt	atgagtccca	aaattcaacc	cttccgatag	ggctgggcct	gacaaaaat	600
atactgggtt	tcctgtttcc	ttttctgatc	attcttacaa	gttatactct	tatttggaa	660
gccctaaaga	aggcttatga	aattcagaag	aacaaaccaa	gaaatgatga	tattaaaaag	720
ataattatgg	caattgtgt	tttcttttc	tttcctgga	ttccccacca	aatattcact	780
tttctggatg	tattgattca	actaggcatc	atacgtgact	gtagaattgc	agatatttg	840
gacacggcca	tgcctatcac	catttgtata	gcttatttt	acaattgcct	gaatcctt	900
ttttatggct	ttctggggaa	aaaattaaa	agatatttc	tccagcttct	aaaatataatt	960
cccccaaaag	ccaaatccca	ctcaaacc	tcaacaaaa	tgagcacgct	ttcctaccgc	1020
ccctcagata	atgtaagctc	atccaccaag	aagcctgcac	catgtttga	ggttgagtga	1080

<210> 90  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 90

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 91

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 91

ccaagaaatg atgatattaa aaagataatt atggc

35

<210> 92

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 92

ctccttcgtt cctcctatcg ttgtcagaag t

31

<210> 93

<211> 1080

<212> DNA

<213> Homo sapiens

<400> 93

atgattctca actcttctac tgaagatgg attaaaagaa tccaagatga ttgtcccaa

60

gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg

120

gtggaaatat ttggaaacag cttgggtgtg atagtcattt acttttatat gaagctgaag

180

actgtggcca gtgttttct tttgaattta gcactggctg acttatgctt tttactgact

240

ttgccactat gggctgtcta cacagctatg gaataccgct ggcctttgg caattaccta

300

tgttaagattt cttcagccag cgtcagttc gccctgtacg ctatgtgtt tctactcact

360

tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg cttcgacgc

420

acaatgcttg tagccaaagt cacctgcac	480
atcatttggc tgctggcagg cttggccagt	
ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagttgt	540
gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat	600
atactgggtt tcctgtttcc tttctgatc attcttacaa gttatactct tatttggaa	660
gcccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag	720
ataattatgg caattgtgct tttcttttc tttcctgga ttccccacca aatattcact	780
tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatatttg	840
gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt	900
ttttatggct ttctgggaa aaaatttaaa agatatttc tccagcttct aaaatatatt	960
cccccaaaag ccaaattcca ctcaaaccctt tcaacaaaaa tgagcacgct ttcctaccgc	1020
ccctcagata atgtaagctc atccaccaag aagcctgcac catgtttga ggttgagtga	1080

<210> 94  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 94

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp			
1	5	10	15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro		
20	25	30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu		
35	40	45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser		
50	55	60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr			
65	70	75	80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe		
85	90	95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu		
100	105	110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
115	120	125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 95	
<211> 26	
<212> DNA	
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cctgcaggcg aaactgactc tggctgaag	29
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gttggatcca cataatgcat tttctc	26
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<211> 1080	
<212> DNA	
<213> Homo sapiens	
<400> 99	
atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaa	60
gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgt	120

gtggaaatat ttggaaacag cttgggtgg atagtcattt acttttatat gaagctgaag	180
actgtggcca gtgttttct tttgaattta gcactggctg acttatgctt ttactgact	240
ttgccactat gggctgtcta cacagctatg gaataccgtt ggcctttgg caattaccta	300
tgtaagattt cttcagccag cgtcagttt aacctgtacg ctagtgtt tctactcact	360
tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccgc cttcgacgc	420
acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt	480
ttgccagcta taatccatcg aaatgttattt ttcattgaga acaccaatat tacagttgt	540
gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat	600
atactgggtt tcctgtttcc tttctgatc attcttacaa gttatggg aattcgaaaa	660
cacttactga agacgaatag ctatgggaag aacaggataa cccgtgacca agttaagaag	720
ataaattatgg caattgtgct tttcttttc tttccctgga ttccccacca aatattcact	780
tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgt	840
gacacggcca tgcctatcac catttgtata gcttattta acaattgcct gaatccttt	900
ttttatggct ttctgggaa aaaatttaaa agatatttc tccagcttct aaaatataatt	960
cccccaaaag ccaaatccca ctcaaaccct tcaacaaaaa tgagcacgct ttcctaccgc	1020
ccctcagata atgtaagctc atccaccaag aagcctgcac catgtttga ggttgagtga	1080

<210> 100

<211> 359

<212> PRT

<213> Homo sapiens

<400> 100

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp			
1	5	10	15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro		
20	25	30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu		
35	40	45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser		
50	55	60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr			
65	70	75	80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys  
210 215 220

Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 101  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 101  
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<210> 102  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 102  
agatcttaag aagataatta tggcaattgt gct 33

<210> 103  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 103  
aattcgaaaa cacttactga agacgaatag ctatggaaag aacaggataa cccgtgacca 60  
ag 62

<210> 104  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 104  
ttaacttggt cacgggttat cctgttcttc ccatagctat tcgtcttcag taagtgtttt 60

<210> 105  
 <211> 1083  
 <212> DNA  
 <213> Homo sapiens

<400> 105  
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 gctggaaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgt 120  
 gtggaaatat ttggaaacag cttgggtgt atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgttttct tttgaattta gcactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggcctttgg caattaccta 300  
 tgtaagattt cttcagccag cgtcagttt aacctgtacg ctatgtgtt tctactcagc 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg cttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcattc atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctggcct gaccaaaaat 600  
 atactgggtt tcctgtttcc tttctgatc attcttacaa gttatactct tatttggaaag 660  
 gcccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgtga tatttttaag 720  
 ataattatgg cagcaattgt gctttcttt ttctttcct ggattccccca ccaaataattc 780  
 acttttctgg atgtattgtat tcaacttaggc atcatacgtg actgtagaat tgcatgatatt 840  
 gtggacacgg ccatgcctat caccattgt atagcttatt ttaacaattt cctgaatcct 900  
 ctttttatg gctttctgg gaaaaaattt aaaagatatt ttctccagct tctaaaatat 960  
 attcccccaa aagccaaatc ccactcaaac ctttcaacaa aatgagcac gctttcctac 1020  
 cggcccttag ataatgtaaag ctcatccacc aagaagcctg caccatgttt tgagggtttag 1080  
 tga 1083

<210> 106  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 106

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
225 230 235 240

Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro  
245 250 255

His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile  
260 265 270

Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr  
275 280 285

Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly  
290 295 300

Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr  
305 310 315 320

Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser  
325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys  
340 345 350

Pro Ala Pro Cys Phe Glu Val Glu  
355 360

<210> 107  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 107  
cccaagcttc cccaggtgta tttgat

26

<210> 108  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 108  
aagcacaatt gctgcataat tatctaaaaa atatcatc

38

<210> 109  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 109	aagataatta tggcagcaat tgtgctttc ttttcttt	39
<210> 110		
<211> 26		
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<223> Novel Sequence		
<400> 110	gttggatcca cataatgcat tttctc	26
<210> 111		
<211> 1344		
<212> DNA		
<213> Homo sapiens		
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	ctgtgccgcc cggggggcgc tctcctcaac agcagcagtg tggcaacct cagctgcgag	120
	ccccctcgca ttgcggagc cgggacacga gaattggagc tggcattag aatcacttt	180
	tacgcagtga tttcctgat gagcgttgg aaaaaatatgc tcatcatcgt ggtcctggaa	240
	ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcaactggc agtcagcgac	300
	ctcctgctgg ctgtggcttg catgccttc accctcctgc ccaatctcat gggcacattc	360
	atcttggca ccgtcatctg caaggcggtt tcctacctca tgggggtgtc tgtgagtgtg	420
	tccacgctaa gcctcgtggc catgcactg gagcgatata gcgcacatctg ccgaccactg	480
	caggcacgag tgtggcagac gcgcctccac gcggctcgcg tgatttagc cacgtggctg	540
	ctgtccggac tactcatggt gccttacccc gtgtacactg tcgtcaacc agtggggcct	600
	cgtgtgtgc agtgcgtgca tcgctggccc agtgcgcggg tccgcccagac ctggtccgta	660
	ctgctgtttc tgctttgtt cttcatccca ggtgtggta tggccgtggc ctacgggctt	720
	atctctcgcg agtctactt agggcttcgc tttgacggcg acagtgcacag cgacagccaa	780
	agcagggtcc gaaaccaagg cgggctgcca gggctgttc accagaacgg gcgttccgg	840
	cctgagactg gcgcgggtgg caaagacagc gatggctgct acgtgcaact tccacgttcc	900
	cggcctgccc tggagctgac ggcgtgacg gctcctggc cggatccgg ctccggccc	960
	acccaggcca agtgcgtggc taagaagcgc gtgaaacgaa tggctgtgt gatcgatgg	1020
	ctttttttc tgtgttgggtt gccagttat agtgcacaaca cgtggcgcc ctggatggc	1080
	ccgggtgcac accgagcact ctcgggtgct cctatctcct tcattcactt gctgagctac	1140

gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgctt tcgccaggcc 1200  
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cccgatgagg accctccac tccctccatt gcttcgctgt ccaggcttag ctacaccacc 1320  
atcagcacac tggccctgg ctga 1344

<210> 112  
<211> 447  
<212> PRT  
<213> Homo sapiens

<400> 112

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly  
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser  
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
85 90 95

Ala Val Ser Asp Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu  
325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly  
435 440 445

<210> 113  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 113  
cagcagcatg cgcttcacgc gcttcttagc ccag

34

<210> 114  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 114  
agaagcgcgt gaagcgcatg ctgctggta tcgtt

35

<210> 115  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 115  
atggagaaaa gaatcaaaag aatgttctat ata

33

<210> 116  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 116  
tatatagaac attctttga ttctttctc cat

33

<210> 117  
<211> 30  
<212> DNA  
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<220>		
<223> Novel Sequence		
<400> 117		
cgctctctgg ccttgaagcg cacgctcagc	30	
<210> 118		
<211> 30		
<212> DNA		
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<400> 118		
gctgagcgtg cgcttcaagg ccagagagcg	30	
<210> 119		
<211> 30		
<212> DNA		
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<223> Novel Sequence		
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cccagaaaaa aggtgaaagt caaagtttc	30	
<210> 120		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
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<223> Novel Sequence		
<400> 120		
gaaaactttg actttcacct ttttcctggg	30	
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<223> Novel Sequence		
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ggggcgccgg tgaaacggct ggtgagc	27	
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<212> DNA		
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	gctcaccaggc cgtttcaccc gcgc	27
<210>	123	
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<212>	DNA	
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<223>	Novel Sequence	
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	cccccttgaaa agcctaagaa cttggtc	30
<210>	124	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
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<223>	Novel Sequence	
<400>	124	
	gatgaccaag ttcttaggct tttcaagggg	30
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<212>	DNA	
<213>	Artificial Sequence	
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<223>	Novel Sequence	
<400>	125	
	gatctctaga atgaacagca catgtattga ag	32
<210>	126	
<211>	35	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Novel Sequence	
<400>	126	
	ctagggttacc cgctcaagga cctctaattc catag	35
<210>	127	
<211>	1296	
<212>	DNA	
<213>	Homo sapiens	

<400> 127  
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acgcggggagc agttcatcgcc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg 120  
ccgggacgcg ccaagctggc cctcgctc accggcgtgc tcatcttcgc cctggcgctc 180  
tttggcaatg ctctgggtt ctacgtggtg acccgagcga aggccatgcg caccgtcacc 240  
aacatctta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc 300  
gtcaccatgc tccagaacat ttccgacaac tggctgggg gtgcatttcatttgc 360  
gtgcatttg tccagtctac cgctgttgtg acagaaatgc tcactatgac ctgcattgt 420  
gtggaaaggc accagggact tgtgcattcct tttaaaatga agtggcaata caccaaccga 480  
agggcttca caatgctagg tgtggctgg ctgggtggcag tcatcgtagg atcacccatg 540  
tggcacgtgc aacaacttga gatcaaataat gacttcctat atgaaaagga acacatctgc 600  
tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catcattgtc 660  
atcctcttcc tcctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa 720  
ctttggataa agaaaagagt tggggatggt tcagtgcctc gaactattca tggaaaagaa 780  
atgtccaaaa tagccaggaa gaagaaacga gctaagatta tgatggtgac agtggtggt 840  
ctcttgctg tgtgctggc accattccat gttgtccata tgatgattga atacagtaat 900  
tttgaaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt 960  
ggattttcca actccatctg taatcccatt gtctatgcat ttatgaatga aaacttcaaa 1020  
aaaaatgttt tgtctgcagt ttgttattgc atagtaataa aaaccttctc tccagcaca 1080  
aggcatggaa attcaggaat tacaatgatg cgaaagaaag caaagtttc cctcagagag 1140  
aatccagtgg aggaaaccaa aggagaagca ttcaagtatg gcaacattga agtcaaattg 1200  
tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctt taggtctgaa 1260  
ctggctgaga atttcctt agacagtggg cattaa 1296

<210> 128  
<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 128

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg  
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg  
20 25 30

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu  
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala  
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr  
65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe  
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu  
100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
195 200 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Lys  
260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Leu Lys Arg His Leu Ala Leu  
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
420 425 430

<210> 129  
<211> 2040  
<212> DNA  
<213> Homo sapiens

<400> 129  
atgggcagcc cctggAACCGG cagcgacggc cccgaggGGG cgccggagcc gccgtggccc 60  
gcgcgtggcgc ctgcgcacga gcgcgcgtgc tcgcctttc ccctggggc gctgggtgccg 120  
gtgaccgctg tgcgcctgtc cctgttcgtc gtcgggggtga gcggcaacgt ggtgaccgtg 180  
atgctgatcg ggcgttacccg ggacatgcgg accaccacca acttgtacct gggcagcatg 240  
gccgtgtccg acctactcat cctgctcggg ctggccgttcg acctgttacccg cctctggcgc 300  
tcgcggccct ggggtttcgg gcccgtgtc tgccgcctgt cccttacgt gggcgaggc 360

tgcacctacg ccacgctgct	gcacatgacc	gcgctcagcg	tcgagcgcta	cctggccatc	420
tgccgccccgc	tccgcgcccgc	cgtcttggtc	accggcgcc	gcgtccgcgc	480
gtgctctggg	ccgtggcgct	gctctctgcc	ggtcccttct	tgttccttgtt	540
caggaccccg	gcatctccgt	agtcccgggc	ctcaatggca	ccgcgcggat	600
cctctcgcc	cgtcgccgcc	tctctggctc	tcgcgggcgc	caccgcgcgtc	660
gggcccaga	ccgcggaggc	cgcggcgctg	ttcagccgcg	aatgcggcc	720
cagctggcg	cgctgcgtgt	catgtgtgg	gtcaccacgg	cctacttctt	780
ctgtgcctca	gcatcctcta	cgggctcatc	gggcgggagc	tgtggagcag	840
ctgcgaggcc	cggccgcctc	ggggcgggag	agaggccacc	ggcagaccaa	900
cgtaagtgg	gccgcccgtgg	ttccaaagac	gcctgcctgc	agtccgcccc	960
gcgcaaacgc	tgggtcccct	tcccctgctc	gcccagctct	gggcggcgct	1020
tttccttattt	cgattccagc	ctccacccgc	cgttacttcc	catccccga	1080
tcctgtcccc	caggagctct	gggggacccc	agggcgctt	gagggtggga	1140
cgattcagta	accagcagtg	cttttccaga	gcctctgaga	ccagaaagga	1200
ttcttaatcc	aaccacctgt	tagatgccac	aaatgaggag	tcctcacagt	1260
agacgaggga	gatttcatta	agctaaaatt	tttttatttaa	tgttaagtga	1320
taaagtaaac	cttgctcgta	tcaaaaagta	aagattgtgc	agacctgttg	1380
ttcaacagag	aacagaaaac	ttgtctccga	agtgggtttgc	tggaaggaag	1440
cggcttgttc	agagaaaatttgc	ctccttctgg	tttatgtcca	gccttgataa	1500
agcctactat	gcagttttaa	agcaagtatc	catgcagcct	gcagcctggt	1560
ggggtgagga	tctgcctagg	tagaagtttt	ctctaattta	ttttgctgtt	1620
gcagatggtt	ctttgtcggg	gtgggggggtt	tatttgcttc	ccaatgctt	1680
ggtgctgtgt	cttatgttgc	agtgggtgt	gttctggcat	ttataatttg	1740
ttccacgttg	gcagaatcat	ttacataaac	acggaagatt	cgcggatgat	1800
cagtacttta	acatcgtcgc	tctgcaactt	ttcttatctga	gcfgcatctat	1860
ctctacaacc	tcatttcaaa	gaagtacaga	gcggcgccct	ttaaactgct	1920
aagtccaggc	cgagaggctt	ccacagaagc	agggacactg	cgggggaaatgt	1980
actggaggag	acacgggtggg	ctacaccgag	acaagcgcta	acgtgaagac	2040

<210> 130

<211> 412

<212> PRT

<213> Homo sapiens

<400> 130

Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu  
1 5 10 15

Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro  
20 25 30

Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu  
35 40 45

Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly  
50 55 60

Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met  
65 70 75 80

Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr  
85 90 95

Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg  
100 105 110

Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His  
115 120 125

Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu  
130 135 140

Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala  
145 150 155 160

Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu  
165 170 175

Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn  
180 185 190

Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu  
195 200 205

Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr  
210 215 220

Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala  
225 230 235 240

Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe  
245 250 255

Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg  
260 265 270

Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly  
275 280 285

Arg Glu Arg Gly His Arg Gln Thr Lys Arg Val Leu Leu Val Val Val  
290 295 300

Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile  
305 310 315 320

Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe  
325 330 335

Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro  
340 345 350

Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys  
355 360 365

Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg  
370 375 380

Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly  
385 390 395 400

Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly  
405 410

<210> 131  
<211> 1344  
<212> DNA  
<213> Homo sapiens

<400> 131  
atggagctgc taaagctgaa ccggagcgtg cagggAACCG gACCCGGGCC gggggcttcc 60  
ctgtgcgcgc cgggggcgccc tctcctcaac agcagcagtg tggcaacct cagctgcgag 120  
ccccctcgca ttgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180

<210> 132

<211> 447

<212> PRT

<213> Homo sapiens

<400> 132

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly  
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser  
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu  
325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Ile Ser Thr Leu Gly Pro Gly  
435 440 445

<210> 133  
<211> 1014  
<212> DNA  
<213> Homo sapiens

<400> 133  
atgaacagca catgtattga agaacagcat gacctggatc actatttgg tcccatgtt 60  
tacatcttg tgattatagt cagcattcca gccaatattt gatctctgtg tgtgtcttc 120  
ctgcaagcaa agaaggaaag tgaacttagga atttacctct tcagttgtc actatcagat 180  
ttactctatg cattaactct ccctttatgg attgattata cttggaaataa agacaactgg 240  
actttctctc ctgccttggt caaaggagt gctttctca tgtacatgaa ttttacagc 300  
agcacagcat tcctcacctg cattgccgtt gatcggtatt tggctgttgc ctacccttg 360  
aagtttttt tcctaaggac aagaagattt gcactcatgg tcagcctgtc catctggata 420

ttggaaacca tcttcaatgc tgtcatgttgc tggaaagatg aaacagttgt tgaatattgc	480
gatgccgaaa agtctaattt tactttatgc tatgacaaat accctttaga gaaatggcaa	540
atcaacctca acttggttcag gacgtgtaca ggctatgcaa taccttttgt caccatcctg	600
atctgtaacc ggaaagtcta ccaagctgtg cgccacaata aagccacgga aaacaaggaa	660
aagaagagaa tcaaaaaact acttgcagc atcacagttt cttttgtctt atgctttact	720
cccttcatg tgatgttgct gattcgctgc atttttagagc atgctgtgaa ctgcgaagac	780
cacagcaatt ctggaaagcg aacttacaca atgtatagaa tcacggttgc attaacaagt	840
ttaaattgtg ttgctgatcc aattctgtac tgttttgtta ccgaaacagg aagatatgat	900
atgtggaata tattaaaatt ctgcactggg aggtgttaata catcacaaag acaaagaaaa	960
cgcatactt ctgtgtctac aaaagatact atgaaattag aggtccctga gtag	1014

<210> 134

<211> 337

<212> PRT

<213> Homo sapiens

<400> 134

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu			
1	5	10	15

Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn		
20	25	30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu Ser Glu		
35	40	45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala		
50	55	60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp			
65	70	75	80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met		
85	90	95

Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg		
100	105	110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg		
115	120	125

Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile  
130 135 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys  
145 150 155 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu  
165 170 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr  
180 185 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln  
195 200 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile  
210 215 220

Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr  
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val  
245 250 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr  
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile  
275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile  
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys  
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu  
325 330 335

Glu

<210> 135

<211> 999

<212> DNA

<213> Homo sapiens

<400> 135  
 atggtaact ccacccaccc tggtatgcac acttctctgc acctctggaa ccgcagcagt 60  
 tacagactgc acagcaatgc cagttagtcc ctggaaaag gctactctga tggagggtgc 120  
 tacgagcaac ttttgtctc tcctgaggtg tttgtgactc tgggtgtcat cagcttgg 180  
 gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240  
 ttttcatct gcagcttggc tgtggctgat atgctggtga gcgttcaaa tggatcagaa 300  
 accattatca tcaccctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360  
 attgataatg tcattgactc ggtgatctgt agctccttgc ttgcattccat ttgcagcctg 420  
 cttcaattt cagttggacag gtactttact atcttctatg ctctccagta ccataacatt 480  
 atgacagtta agcggggttgg gatcagcata agttgtatct gggcagcttgc cacggttca 540  
 ggcattttgt tcatcattta ctcagatagt agtgctgtca tcatctgcct catcaccatg 600  
 ttcttcacca tgctggctct catggcttct ctctatgtcc acatgttccat gatggccagg 660  
 cttcacatata agaggattgc tgcctcccc ggcactggtg ccatccgcca aggtgccaat 720  
 atgaaggaa aaattacattt gaccatcctg attggcgtct ttgttgctg ctggggccca 780  
 ttcttcctcc acttaatattt ctacatctct tgcctcaga atccatattt tgcgtgcttc 840  
 atgtctcaact ttaacttgta tctcatactg atcatgtgta attcaatcat cgatcctctg 900  
 atttatgcac tccggagtca agaactgagg aaaaccttca aagagatcat ctgttgctat 960  
 cccctggag gcctttgtga ctgtcttagc agatattaa 999

<210> 136  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 136

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp  
 1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly  
 20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro  
 35 40 45

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu  
 50 55 60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr  
65 70 75 80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser  
85 90 95

Asn Gly Ser Glu Thr Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr  
100 105 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val  
115 120 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala  
130 135 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile  
145 150 155 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala  
165 170 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala  
180 185 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met  
195 200 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys  
210 215 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn  
225 230 235 240

Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val  
245 250 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro  
260 265 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr  
305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
325 330

<210> 137  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 137  
gccaatatga agggaaaaat taccttgacc atc 33

<210> 138  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 138  
ctccttcggt ctcctatcg ttgtcagaag t 31

<210> 139  
<211> 1842  
<212> DNA  
<213> Homo sapiens

<400> 139  
atggggccca ccctagcggt tcccacccccc tatggctgta ttggctgtaa gctacccag 60  
ccagaatacc caccggctct aatcatcttt atgttctgct cgatggttat caccatcggt 120  
gtagacctaa tcggcaactc catggcatt ttggctgtga cgaagaacaa gaagctccgg 180  
aattctggca acatttcggt ggtcagtctc tctgtggccg atatgctggt ggccatctac 240  
ccataccctt ttagtctgca tgccatgtcc attggggctt gggatctgag ccagttacag 300  
tgccagatgg tcgggttcat cacaggctg agtgtggctg gctccatctt caacatcggt 360  
gcaatcgcta tcaaccgtta ctgctacatc tgccacagcc tccagttacga acggatcttc 420  
agtgtgcgca atacctgcat ctacctggtc atcacctgga tcatgaccgt cctggctgtc 480  
ctgccccaca tgtacattgg caccatcgag tacgatcctc gcacccatcac ctgcacatctc 540  
aactatctga acaaccctgt cttcactgtt accatcgatc gcatccactt cgtccctccct 600  
ctcctcatcg tgggtttctg ctacgtgagg atctggacca aagtgtggc ggcccggtgac 660

cctgcagggc	agaatcctga	caaccaactt	gctgaggttc	gcaattttct	aaccatgttt	720
gtgatcttcc	tcctcttgc	agtgtgctgg	tgccctatca	acgtgctcac	tgtcttggtg	780
gctgtcagtc	cgaaggagat	ggcaggcaag	atccccact	ggcttatct	tgcagcctac	840
ttcatacgct	acttcaacag	ctgcctcaac	gctgtgatct	acgggctcct	caatgagaat	900
ttccgaagag	aatactggac	catttccat	gctatgcggc	accctatcat	attttccct	960
ggcctcatca	gtgatattcg	tgagatgcag	gaggcccgta	ccctggcccg	cgcggcgcc	1020
catgctcgcg	accaagctcg	tgaacaagac	cgtgcccattg	cctgtcctgc	tgtggaggaa	1080
accccgatga	atgtccggaa	tgttccatta	cctggtgatg	ctgcagctgg	ccaccccgac	1140
cgtgcctctg	gccaccctaa	gccccattcc	agatcctct	ctgcctatcg	caaatctgcc	1200
tctacccacc	acaagtctgt	ctttagccac	tccaaggctg	cctctggtca	cctcaaggct	1260
gtctctggcc	actccaagcc	tgcctctggt	caccccaagt	ctgcactgt	ctaccctaag	1320
cctgcctctg	tccatttcaa	gggtgactct	gtccatttca	agggtgactc	tgtccatttc	1380
aagcctgact	ctgttcattt	caagcctgct	tccagcaacc	ccaagccat	cactggccac	1440
catgtctctg	ctggcagcca	ctccaagtct	gccttcagtg	ctgcaccag	ccaccctaaa	1500
cccatcaagc	cagctaccag	ccatgctgag	cccaccactg	ctgactatcc	caagcctgcc	1560
actaccagcc	accctaagcc	cgctgctgct	gacaaccctg	agctctctgc	ctcccattgc	1620
cccgagatcc	ctgccattgc	ccaccctgtg	tctgacgaca	gtgacctccc	tgagtccggcc	1680
tctagccctg	ccgctgggccc	caccaaggct	gctgccagcc	agctggagtc	tgacaccatc	1740
gctgaccttc	ctgaccctac	tgttagtca	accagtagcca	atgattacca	tgtatgtcgtg	1800
gttgtttagt	ttgaagatga	tcctgatgaa	atggctgtgt	ga		1842

<210> 140

<211> 613

<212> PRT

<213> Homo sapiens

<400> 140

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys  
 1 5 10 15

Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe  
 20 25 30

Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met  
 35 40 45

Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn  
50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr  
65 70 75 80

Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu  
85 90 95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val  
100 105 110

Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys  
115 120 125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn  
130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val  
145 150 155 160

Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr  
165 170 175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile  
180 185 190

Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr  
195 200 205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln  
210 215 220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe  
225 230 235 240

Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu  
245 250 255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro  
260 265 270

Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys  
275 280 285

Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu  
290 295 300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro  
305 310 315 320

Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala  
325 330 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala  
340 345 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val  
355 360 365

Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly  
370 375 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala  
385 390 395 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly  
405 410 415

His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro  
420 425 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly  
435 440 445

Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser  
450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His  
465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr  
485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr  
500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala  
515 520 525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro  
530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala  
545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu  
565 570 575

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser  
580 585 590

Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro  
595 600 605

Asp Glu Met Ala Val  
610

<210> 141  
<211> 1842  
<212> DNA  
<213> Homo sapiens

<400> 141  
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Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn  
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Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr  
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Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu  
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Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val  
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Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn  
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Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val  
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Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile  
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His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val  
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Pro Leu Pro Gly Asp Ala Ala Gly His Pro Asp Arg Ala Ser Gly  
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His Pro Lys Pro His Ser Arg Ser Ser Ala Tyr Arg Lys Ser Ala  
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Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly  
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His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro  
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Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala  
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Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser  
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Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His  
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His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr  
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Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr  
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Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala  
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Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala  
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